

Identification of Defects in the Fibrillin Gene and Protein

in Individuals with the Marfan Syndrome
and Related Disorders

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The Marfan syndrome is an autosomal dominant disorder with pleiotropic manifestations that involve the cardiovascular, ocular, and skeletal systems. Through a number of investigational approaches, the gene encoding for fibrillin, the FBN1 gene on chromosome 15, has been identified as the defective gene causing the Marfan syndrome. Fibrillin is the large glycoprotein with a repetitive domain structure and is a major protein component of microfibrils, a fibrillar system closely associated with elastin in connective tissue. Mutational analysis of defects in the FBN1 gene in patients with the Marfan syndrome has revealed that most mutations are private or unique in an affected individual or family. Analysis of fibrillin protein or gene defects in individuals with related phenotypes has revealed that a perinatal lethal syndrome, termed neonatal Marfan syndrome, is due to FBN1 gene mutations. In addition, fibroblast cell strains from a subset of patients with idiopathic scoliosis have fibrillin protein defects. Last, fibroblasts from calves affected with bovine Marfan syndrome display defects in the fibrillin protein. These studies have wide-ranging implications in the diagnosis, treatment, and prevention of Marfan syndrome and related disorders. (Texas Heart Institute Journal 1994;21:22-9)

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The Marfan syndrome is an autosomal dominant disorder with cardiovascular, skeletal, and ocular complications. The disorder has an estimated prevalence of 1 per 10,000 population.¹ Approximately one quarter of patients are born to parents who are not clinically affected, and are thought to result from new mutations in the parental germline. The Marfan syndrome shows high penetrance, and variability in the clinical expression of the disease is common, both between and within families.

The life-threatening complications of the Marfan syndrome are related to the cardiovascular complications. Before the advent of cardiovascular surgery to correct these problems, the life expectancy of an affected patient was greatly decreased, with an average age at death of 32 years.² The most serious cardiovascular problem is progressive dilatation of the ascending aorta, which can lead to dissection or rupture if not surgically corrected.³⁻⁵ The majority of patients with the Marfan syndrome also have mitral valve abnormalities, most commonly mitral valve prolapse, but also mitral regurgitation.^{6,7}

The skeletal features of the disorder are the most outwardly striking characteristics of the syndrome. Affected individuals typically are very tall, with long arms and legs (dolichostenomelia) and long, thin fingers (arachnodactyly). In addition, they can have skeletal features such as pectus deformities, scoliosis, high-arched palate, pes planus, and joint hypermobility. Cardinal manifestations involving the eye include lens dislocation (ectopia lentis), myopia, and retinal detachment.

In the past few years, intensive work by a number of groups has identified the defective gene causing the Marfan syndrome, the fibrillin or FBN1 gene. Characterizations of mutations in this gene have provided information about the structural domains of the fibrillin protein important for the integrity of the connective tissue. In addition, further work has defined the spectrum of phenotypes associated with FBN1 gene mutations. These studies have wide-ranging implications for the prevention, diagnosis, and treatment of these disorders.

Elastin and Microfibrils

Initial work to elucidate the pathogenesis of the Marfan syndrome involved histopathologic examination of aortas from individuals with the Marfan syndrome. These examinations revealed cystic medial necrosis characterized by focal loss or fragmentation of elastic fibers.⁸ Abnormal elastic fibers were observed in other tissues (including lung and skin) from patients with the Marfan syndrome.^{9,10} Biochemical analysis of aortic tissue confirmed substantial reduction in elastin content and revealed a 50% decrease in the desmosine (elastin-specific cross-links) content of the isolated elastin.⁸ All these results suggested a defect in the formation of elastin fibers. Initially, attention focused on the gene for elastin, the major protein in the elastic fiber. A candidate gene approach was not successful in excluding elastin as the candidate gene, due to a lack of polymorphisms in or around the gene.

The 2 major components of the elastic fiber are an amorphous core of elastin and a matrix of microfibrils that surrounds the amorphous core (Fig. 1). Microfibrils are approximately 10-nm fibers that appear on the periphery of the amorphous core of elastin, but also appear in tissues without elastin.^{11,12} Microfibrils appear to play a role in the formation of elastin fibers during development, by providing a scaffold upon which newly synthesized elastin is deposited. The most striking accumulation of microfibrils (without elastin present) is found in the zonule of Zinn, the suspensory ligament of the eye that holds the lens in place. Because microfibrils were found both in the elastic fibers and in the suspensory ligament of the eye, the protein components of the microfibrils became candidates for the defective gene product causing the Marfan syndrome.

In 1986, the major protein component of microfibrils was identified and termed fibrillin.¹² Fibrillin

is a large glycoprotein (350 kD) that is found both in microfibrils associated with elastin and in microfibrils not associated with elastin. The protein is found in a wide variety of tissues, including those of the skin, lung, kidney, vessels, cartilage, tendon, muscle, cornea, and suspensory ligament of the eye. Once the major protein component of microfibrils had been identified, the gene that encodes for fibrillin became a major candidate for the defective gene causing the Marfan syndrome.

Identification of the Genetic Defect

In the late 1980s a number of approaches were used to identify the genetic defect causing the Marfan syndrome (Fig. 2). An international consortium of investigators was carrying out genetic linkage analysis with anonymous polymorphic probes to map the chromosomal locus for the genetic defect causing the Marfan syndrome. Other investigators endeavored to clone, characterize, and determine the chromosomal location of the fibrillin gene. Last, biochemical studies were under way to discover specific defects in the structure, synthesis, and processing of fibrillin by cells from Marfan patients.

The 1st biochemical data to support fibrillin as the defective gene product causing the Marfan syndrome came from work by the late D. Hollister and colleagues.¹³⁻¹⁵ Their work strengthened the hypothesis that fibrillin was the defective gene causing the Marfan syndrome by demonstrating decreased immunofluorescence of anti-fibrillin antibody-stained dermal biopsies and cultured fibroblasts from Marfan syndrome patients. Further biochemical evidence that fibrillin was the defective gene product came from our studies of the synthesis, secretion, and processing of fibrillin by dermal fibroblasts from Marfan patients. These studies showed 3 metabolic defects in fibrillin processing by dermal fibroblasts from Marfan patients: decreased fibrillin synthesized by the cell, inefficient secretion of fibrillin, and de-

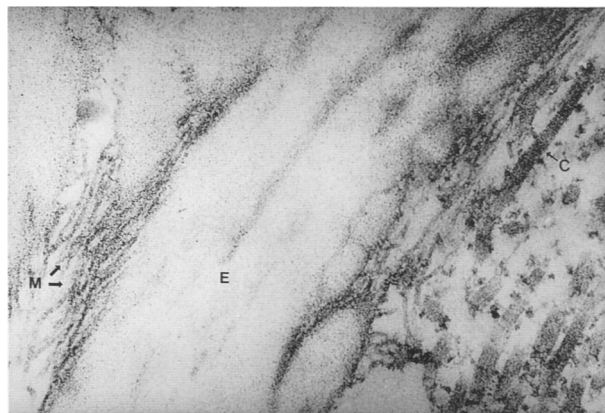


Fig. 1 Electron microscopic examination of microfibrils (M) around the amorphous core of an elastic fiber (E) in human skin. Larger collagen fibers (C) can be seen.

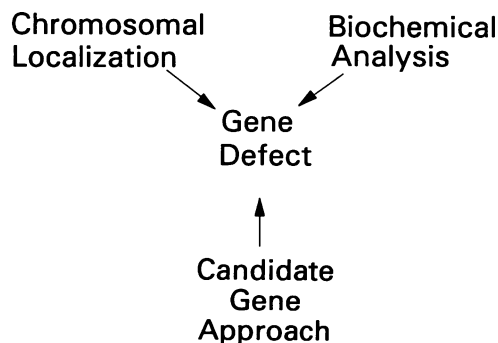


Fig. 2 Three scientific approaches pursued by different investigators to identify the genetic defect causing the Marfan syndrome.

creased incorporation of fibrillin into the pericellular matrix, presumably in the form of microfibrils (Fig. 3).^{16,17}

By 1990, researchers participating in the international consortium reported exclusion of 75% of the human genome as the site of the Marfan syndrome locus.¹⁸ In 1991, Finnish researchers reported linkage of the Marfan syndrome to the long arm of chromosome 15, 15q15.23.¹⁹ Subsequent studies further defined the locus and showed that all Marfan families studied were linked to this region, i.e., there was no evidence of genetic heterogeneity.^{20,21}

The final steps in determining the defective gene causing the Marfan syndrome came with the cloning of the partial cDNA of fibrillin by 2 groups.^{22,23} Polymorphic markers within the gene were shown to be closely linked to the Marfan syndrome without recombination.^{22,24} In addition, the gene was mapped to 15q15.21, the same chromosomal location to which Marfan syndrome had been mapped using random genomic probes.²² The final proof came with the identification of a de novo mutation causing the disease in 2 patients with sporadic disease.²⁴

The Fibrillin Gene and Protein Structure. The complete cDNA sequence encoding fibrillin was reported in 1993 by 2 research groups.^{25,26} The cDNA sequence predicts a cysteine-rich glycoprotein with a repetitive domain structure, as shown in Fig. 4. The

fibrillin gene is relatively large (approximately 110 kb). The cDNA is encoded in 64 exons, with almost every cysteine-rich motif encoded by its own exon.²⁶

The protein contains 47 repeats that have homology to epidermal growth factor (EGF), 43 of which are predicted to bind calcium, due to the presence of a calcium-binding motif.^{27,28} Each of these repeats contains 6 cysteines that are inferred to form the same disulfide bonds as EGF, i.e., disulfide bonds between the 1st and 3rd, 2nd and 4th, and 5th and 6th cysteines. In addition, the protein has repeats with homology to domains found in the transforming growth factor β 1 binding protein (TGF β 1 binding protein).²⁹ These domains are also cysteine rich, containing 8 cysteines each. Fibrillin has other cysteine-rich domains that are variants of the EGF and TGF β 1 binding protein motifs (hybrid motifs). Last, fibrillin has 3 unique domains: an amino-terminal domain, a carboxy-terminal domain, and a proline-rich domain found towards the amino-terminal end of the protein. The protein has a number of putative sites for N-linked glycosylation.

Characterization of Mutations in the Fibrillin Gene. A number of mutations in the fibrillin gene have been identified in patients with the Marfan syndrome (Table I^{24,25,30-36}). With the exception of the 1st de novo mutation identified in 2 unrelated affected individuals, all mutations have been private

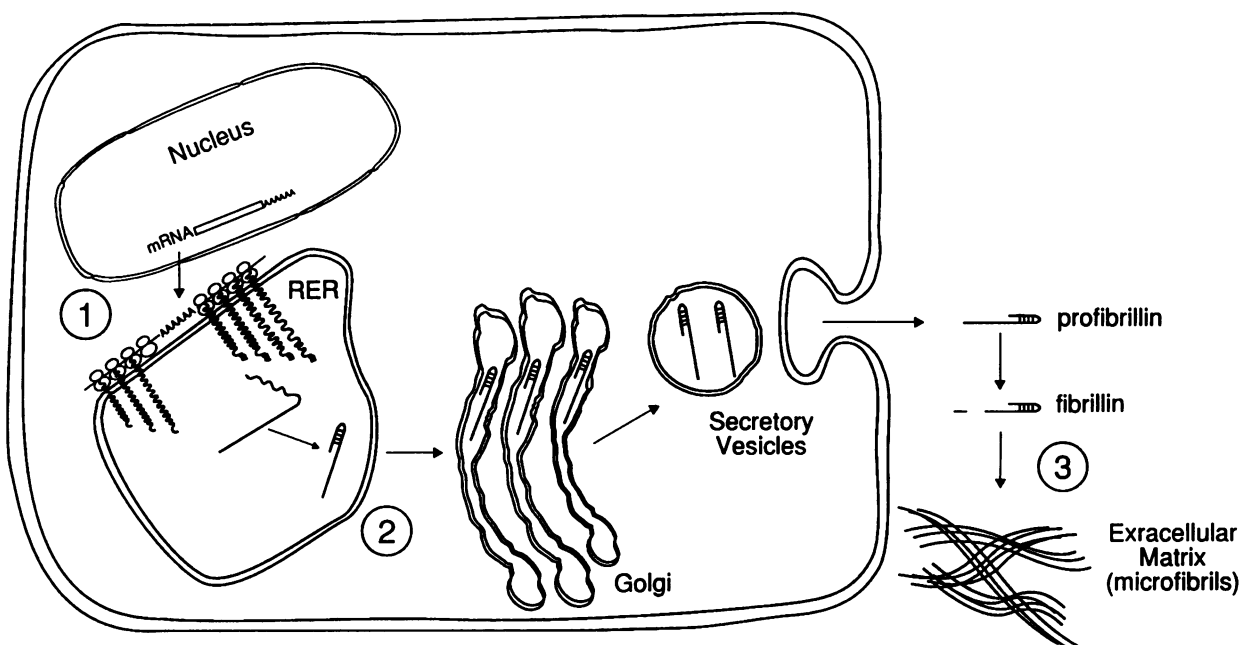


Fig. 3 Diagrammatic representation of fibrillin synthesis, secretion, proteolytic conversion, and microfibril formation by human dermal fibroblasts. The circled numbers indicate the approximate location of defects in the synthesis (1), secretion (2), and matrix incorporation (3) of fibrillin in dermal fibroblasts from individuals with the Marfan syndrome.

RER = rough endoplasmic reticulum

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or unique in every family. Currently, there is no correlation between the location of the mutation and the resulting severity of the Marfan syndrome or specific systems affected.

All missense mutations identified are predicted to disrupt EGF-like domains that bind calcium.^{24,30-33} Four of the missense mutations involve substitution of 1 of the highly conserved cysteines in the EGF-

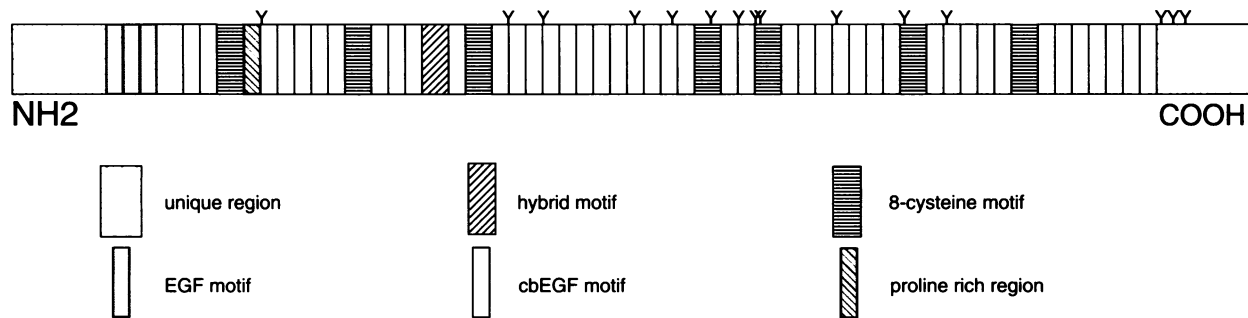


Fig. 4 Diagrammatic representation of the fibrillin protein structure based on the cDNA sequence. The different domains observed in the fibrillin protein are labeled in the figure legend. The Y characters above the boxes indicate potential sites of N-linked glycosylation based on the amino acid sequence.

EGF = epidermal growth factor; cbEGF = calcium-binding epidermal growth factor

TABLE I. Identified Mutations in the FBN1 Gene in Marfan Patients

SEQUENCE ALTERATIONS*	AMINO ACID CHANGES*	PREDICTED EFFECT ON PROTEIN
Missense Mutations		
G716C	R239P	Disrupt secondary structure of EGF-like domain ²⁴
G4226C	C1409S	Disrupt secondary structure of EGF-like domain ³⁰
G1052C	C351S	Disrupt secondary structure of EGF-like domain ³¹
T2293C	C765R	Disrupt secondary structure of EGF-like domain ³¹
G3968C	C1323S	Disrupt secondary structure of EGF-like domain ³¹
A-1052T	N-351I	Disrupt Ca ⁺⁺ binding to EGF-like domain ³²
A-527C	D-176A	Disrupt Ca ⁺⁺ binding to EGF-like domain ³²
A3737G	N1246S	Disrupt Ca ⁺⁺ binding to EGF-like domain ³³
Nonsense Mutations		
G5574A	W1858X	Premature termination of protein translation ³⁴
Insertion/Deletions		
2444 ins TTCA	-	Premature termination of protein translation ³²
del -2530 to -2448 (splicing error, G +1 to A)	-	Premature termination of protein translation ³²
del 4762 to 5127 (genomic deletion)	-	Deletion of 3 EGF-like domains with protein translation maintained ³⁴
del 6664 to 6787 (splicing error, G +1 to C)	-	Deletion of 1 EGF-like domain with protein translation maintained ³⁵
del 3620 to 3685 (T3645G)	Y1215X	Deletion of 1 EGF-like domain with protein translation maintained ³⁶

*Nucleotide and amino acid numbering as used by Corson.²⁵

like domains, therefore predicted to disrupt the secondary structure of the EGF-like domain by preventing proper disulfide bonding. Specific residues within the EGF-like domains have been shown to be critical for calcium binding.^{27,28,37,38} Three missense mutations (N1246S, N-351I, and D-176A) disrupt these amino acids for calcium binding. The last missense mutation (R239P) does not disrupt an amino acid critical for calcium binding, but the substitution of a proline residue for an arginine would disrupt the secondary structure of the domain. Although these missense mutations are predicted to affect the binding of calcium to the EGF-like domain, the role that calcium binding plays in fibrillin function has yet to be elucidated.

Three splicing errors have been identified^{32,35,36} as the causative mutation in 3 unrelated Marfan patients. Two of these mutations delete EGF-like domains and leave the reading frame of the protein intact,^{35,36} whereas 1 deletes an EGF-like domain and disrupts the reading frame, leading to a truncated protein.³² Two of these splicing errors are due to mutations at the splice donor site.^{32,35} The last splicing error results from a nonsense mutation at position +26 of the deleted exon.³⁶ Surprisingly, the reading frame of the protein is maintained despite the abnormally spliced exon.

A number of mutations result in the synthesis of a truncated protein. A nonsense mutation in the carboxy terminus is predicted to shorten the protein by 116 amino acids.³⁴ An insertion of 4 amino acids at nucleotide 2444 leads immediately to a premature stop.³² Last, a genomic deletion results in deletion of 366-bp from the fibrillin message, producing an in-frame deletion of 122 amino acids.

A number of conclusions can be drawn from the mutational analysis. First, disruption of the secondary structure of EGF-like domains (e.g., disrupting disulfide pairing by mutating 1 of the cysteines) can cause the phenotypic manifestations of the Marfan syndrome. Second, mutations that disrupt the calcium-binding motif in the EGF-like domains can produce the disease. Third, selective deletion of 1 of these domains can also result in the disorder. Last, truncation of the protein, even within the unique carboxy-terminal domain, can produce disease. Surprisingly, no large genomic rearrangements leading to a nonexpressed or null allele have been identified, raising the possibility that a true null allele does not cause typical Marfan syndrome.

Spectrum of Phenotypes

Associated with Fibrillin Protein Defects

The varied clinical features of the Marfan syndrome have led to speculation that isolated features of this disorder (or related syndromes) may be due to mutations in the FBN1 gene. One Marfan-related disorder

has been shown to be due to mutations in the fibrillin gene, dominantly inherited ectopia lentis.³⁹ Initial studies of families with dominantly inherited mitral valve prolapse or annuloaortic ectasia have not shown linkage to the FBN1 gene.

We have been interested in investigating the role of fibrillin in a number of clinical disease states. Screening the greater than 8 kb of the fibrillin cDNA for mutations that cause the Marfan syndrome presents a formidable task. Instead, we have relied on biochemical assessment of fibrillin synthesis and processing by using dermal fibroblasts from affected individuals as a screen for possible FBN1 mutations (see Fig. 3). If a protein defect is identified, the fibrillin cDNA is analyzed for a mutation. Using this protocol, we have assessed the role of FBN1 mutations in the following disorders: neonatal Marfan syndrome, adolescent idiopathic scoliosis, and an animal model of the Marfan syndrome. In addition, we are in the process of investigating the role of fibrillin in the pathogenesis of isolated thoracic aortic aneurysms and a number of other disorders.

Neonatal Marfan Syndrome. This is a sporadic, perinatal, lethal syndrome with features of the Marfan syndrome along with manifestations not observed in classic Marfan syndrome.⁴⁰⁻⁴⁴ Affected children are born with severe cardiovascular problems, including mitral valve regurgitation and progressive aortic root dilatation, and with ocular and skeletal features typical of the Marfan syndrome (Fig. 5). In addition, these patients have congenital contractures, atypical facies, loose, redundant skin, and pulmonary emphysema. These children usually die within the 1st year of life. This more severe and complex phenotype, exhibiting features not typically found in Marfan patients, leads to questions about the molecular defect causing neonatal Marfan syndrome. In our study of an infant with this syndrome, we explanted dermal fibroblasts and found that these cells secreted fibrillin inefficiently, suggesting a mutation in the FBN1 gene. The fibrillin cDNA from the patient's fibroblasts was screened for a mutation and a unique 3-bp insertion was identified between bases 480 and 481 or 481 and 482 of the fibrillin cDNA.^{45,46} The insertion maintains the reading frame of the fibrillin protein but inserts an additional cysteine into 1 of the EGF-like repeats. Therefore, we concluded that neonatal Marfan syndrome was due to mutations in the FBN1 gene. We now are investigating why a mutation in this region of the fibrillin protein results in such severe disease.

Adolescent Idiopathic Scoliosis. Scoliosis is 1 of the pleiotropic manifestations of the Marfan syndrome, raising the possibility that individuals with isolated adolescent idiopathic scoliosis may have defects in fibrillin. To answer this question, we have collaborated with Nancy Hadley-Miller, Baylor College of

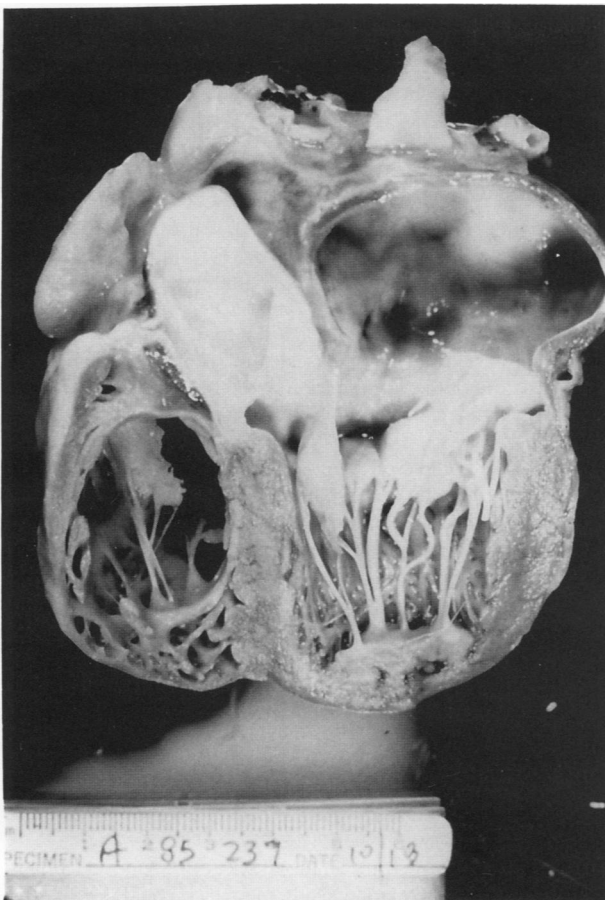


Fig. 5 Heart at autopsy of a patient with neonatal Marfan syndrome who died at the age of 17 months. Note the enlarged left atrium, ventricles, and aortic root, and the redundant chordae and leaflets of the mitral valve.

Medicine, to study fibrillin processing by fibroblasts explanted from the ligamentum flavum of individuals with idiopathic scoliosis. We identified a small subset of these patients (4 out of 23, or 17%) who have a defect in fibrillin processing. The specific defect identified in all patients was failure of fibrillin to incorporate into the pericellular matrix surrounding the cells.⁴⁷ Fibrillin cDNA from the cell lines that demonstrate a fibrillin defect is now being screened for a FBN1 mutation. The preliminary data suggest that fibrillin defects have a role in the causation of idiopathic scoliosis.

Bovine Marfan Syndrome. The 1st potential animal model of the Marfan syndrome was recently identified by veterinarians at Washington State University.⁴⁸ Bovine Marfan syndrome resembles human Marfan syndrome in that affected cows have skeletal anomalies (dolichostenomelia, joint hypermobility), ocular findings (ectopia lentis), and cardiovascular lesions (aortic root dilatation and rupture) that are similar to features observed in human beings with Marfan syndrome (Fig. 6). To determine if fibrillin processing was abnormal, we obtained dermal fibro-



Fig. 6 Bovine Marfan syndrome. This calf was diagnosed as affected based upon hypermobility of distal limbs, dolichostenomelia, ectopia lentis, and aortic root dilatation.

blasts from affected calves and age-matched controls.⁴⁹ Metabolic labeling studies of fibrillin showed clearly that cells from affected calves did not incorporate fibrillin into the pericellular matrix, whereas cells from normal calves demonstrated normal incorporation of fibrillin. In conclusion, these results suggest that the bovine Marfan syndrome is also caused by a mutation in fibrillin, leading to defective incorporation into microfibrils.

Conclusion

Research over the past 4 years has identified the FBN1 or fibrillin gene as the defective gene causing the Marfan syndrome. Characterization of mutations in the FBN1 gene in individuals with the disorder has provided some preliminary information about the functional significance of some regions of the fibrillin protein, but further work is needed to complete our understanding of how fibrillin defects cause the Marfan syndrome. Last, work is in progress to determine the full range of clinical disease associated with FBN1 mutations.

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